

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 14:18:50 ; Search time 29.33 seconds
(without alignments)
1758.319 Million cell updates/sec

Title: US-08-883-036a-2

Perfect score: 2327
Sequence: 1 MEORQONAPASGARRKRRHP.....HLLSGKMYLEGNADSAMS 440

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhcl:*
8: sp_mammal:*
9: sp_mhcl:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_vertebrate:*
15: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2327	100.0	440	014763	014763 homo sapien
2	2313	99.4	440	015531	015531 homo sapien
3	2151.5	92.5	411	015508	015508 homo sapien
4	2138.5	91.9	411	014720	014720 homo sapien
5	2137.5	91.9	411	015517	015517 homo sapien
6	1061.5	45.6	468	000220	000220 homo sapien
7	869	37.3	386	09UBN6	09UBN6 homo sapien
8	855	35.7	386	09Y604	09Y604 homo sapien
9	588	25.3	381	09QZM4	09QZM4 mus musculu
10	580	24.9	381	09JTL6	09JTL6 mus musculu
11	565	24.3	385	0109JL5	0109JL5 mus musculu
12	488.5	21.0	368	0130JL5	0130JL5 mus musculu
13	474.5	20.4	368	0130JL5	0130JL5 mus musculu
14	467	20.1	299	014798	014798 homo sapien
15	464.5	20.0	368	0130JL5	0130JL5 mus musculu
16	441	19.0	259	014755	014755 homo sapien
17	217	9.3	426	014865	014865 homo sapien
18	203	8.7	418	000275	000275 homo sapien
19	200.5	8.6	387	09PVD4	09PVD4 xenopus lae

20	199.5	8.6	314	4	014293	014293 homo sapien
21	195	8.4	331	6	09TSM4	09TSM4 macaca fasc
22	191	8.2	380	4	000280	000280 homo sapien
23	179	7.7	327	6	097491	097491 ovis aries
24	175.5	7.5	302	13	09PUS0	09PUS0 salvelinus
25	174	7.5	283	6	09X528	09X528 cercopithec
26	172	7.4	439	4	016042	016042 homo sapien
27	170	7.3	348	14	057277	057277 monkeypox v
28	170	7.3	372	4	000279	000279 homo sapien
29	168.5	7.2	263	6	09X560	09X560 oryctolagus
30	168.5	7.2	319	6	09TV79	09TV79 oryctolagus
31	168.5	7.2	320	6	09X529	09X529 oryctolagus
32	168	7.2	348	14	057108	057108 monkeypox v
33	167.5	7.2	349	14	057291	057291 monkeypox v
34	167.5	7.2	349	14	057100	057100 monkeypox v
35	167.5	7.2	349	14	057102	057102 monkeypox v
36	167.5	7.2	459	11	062327	062327 mus musculu
37	166	7.1	348	14	057103	057103 monkeypox v
38	164.5	7.1	349	14	057099	057099 monkeypox v
39	161.5	6.9	349	14	057100	057100 monkeypox v
40	161.5	6.9	351	14	057117	057117 monkeypox v
41	161	6.9	417	11	09Z0W1	09Z0W1 mus musculu
42	158.5	6.8	482	11	088734	088734 mus musculu
43	157.5	6.8	401	13	09PRG7	09PRG7 xenopus lae
44	155	6.7	189	6	097530	097530 canis faml
45	154.5	6.6	616	4	09Y606	09Y606 homo sapien

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	440 AA.
014763	014763			
AC	014763			
DT	01-JAN-1998 (TREMBL)	05, Created		
DT	01-JAN-1998 (TREMBL)	05, Last sequence update		
DT	01-OCT-2000 (TREMBL)	15, Last annotation update		
DE	APOPTOSIS INDUCING RECEPTOR TRAIL-R2.			
GN	TRAILR2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97459925; Pubmed=931198.			
RA	Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,			
RA	Bolant M., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,			
RA	Goodwin R.G., Rauch C.T.,			
RT	"TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";			
RL	EMBO J. 16:5386-5397(1997).			
DR	EMBL; AF016849; AAC51778.1; -			
DR	HSSP; P19438; INCF.			
DR	INTERPRO; IPR000488; -			
DR	INTERPRO; IPR001368; -			
DR	PFAM; PF00020; TNFR_c6; 2.			
DR	PFAM; PF00531; death; 1.			
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.			
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.			
SO	SEQUENCE 440 AA; 47850 MW; 603005AF2A8B4870 CRC64;			
Query Match	100.0%;	Score 2327;	DB 4;	Length 440;
Best Local Similarity	100.0%;	Pred. No. 1.7e-180;		
Matches 440; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1	MEORQONAPASGARRKRRGPRRARGARPRVPTLVVAVALLVSAESALTIPOD	60	
DB	1	MEORQONAPASGARRKRRGPRRARGARPRVPTLVVAVALLVSAESALTIPOD	60	
OY	61	LAPQORAPQQRSSPSGGLCPGHNISDGRDCISCKYGQDYSTHWNLLFLCLTRCD	120	

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Db 61 LAPQORAPPOQRSSPSEGLCPGHHISEDRDCISCKYGQDYSTHWNDDLFCRLCTRCD 120
121 SGEVELSPCTTTNTNTVOCCEGTFRDEDSPEMKCKRTGCGRGVAVGDDCTPMSDIECVH 180
121 SGEVELSPCTTTNTNTVOCCEGTFRDEDSPEMKCKRTGCGRGVAVGDDCTPMSDIECVH 180
181 KESGTHSGEPAPAVEETVTSPTGTPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
181 KESGTHSGEPAPAVEETVTSPTGTPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
Db 241 LPTKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSIILOPTQVPEQEMEVOEPAEPTGV 300
241 LPTKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSIILOPTQVPEQEMEVOEPAEPTGV 300
Db 301 NMLSPGSEHLLPEPAERERORRLVLPANEGDPTETLRQCFFDFADLVFPDSWEPLMRK 360
301 NMLSPGSEHLLPEPAERERORRLVLPANEGDPTETLRQCFFDFADLVFPDSWEPLMRK 360
Db 361 LGIMDNEIKYAKAEAGHDTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 420
361 LGIMDNEIKYAKAEAGHDTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 420
Db 421 HLISGKFMYLEGNADSAMS 440
421 HLISGKFMYLEGNADSAMS 440

RESULT 2
015531 PRELIMINARY; PRT; 440 AA.
ID 015531;
AC 015531;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE APOPTOSIS INDUCING PROTEIN.
GN TRICK2B OR DR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Screation G.R., Mongkolkeasapaya J., Xu X., Cowper A.E., McMichael A.J.,
RA Bell A.J.;
RA Tschopp J.;
RL FEBS Lett. 0:0-0(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;
RT "Genomic Structure and Mutation Analyses of the DR5/TRAIL receptor 2
RT Gene in Colorectal Carcinoma.";
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF018658; AAB70578.1; -
DR EMBL; AF016266; AAB81180.1; -
DR EMBL; AB014718; BAA33723.1; -
DR EMBL; AB014710; BAA33723.1; JOINED.
DR EMBL; AB014712; BAA33723.1; JOINED.
DR EMBL; AB014711; BAA33723.1; JOINED.
DR EMBL; AB014713; BAA33723.1; JOINED.
DR EMBL; AB014714; BAA33723.1; JOINED.
DR EMBL; AB014715; BAA33723.1; JOINED.
DR EMBL; AB014716; BAA33723.1; JOINED.
DR EMBL; AB014717; BAA33723.1; JOINED.
DR HSSP; P19438; INCF.
DR INTERPRO; IPR000488; -
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_C6; 2.
DR PFAM; PF00531; Death; 1.

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DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 440 AA; 4789 MW; 7E9367DF3ED24DDE CRC64;

Query Match 99.4%; Score 2313; DB 4; Length 440;
Best Local Similarity 99.5%; Pred. No. 2,3e-179;
Matches 438; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEORGONAPASGARRKHGPRREARGARPGPRVPTVLYVVAVLLVSASALITQOD 60
1 MEORGONAPASGARRKHGPRREARGARPGPRVPTVLYVVAVLLVSASALITQOD 60
Db 1 MEORGONAPASGARRKHGPRREARGARPGPRVPTVLYVVAVLLVSASALITQOD 60
1 MEORGONAPASGARRKHGPRREARGARPGPRVPTVLYVVAVLLVSASALITQOD 60
Db 61 LAPQORAPPOQRSSPSEGLCPGHHISEDRDCISCKYGQDYSTHWNDDLFCRLCTRCD 120
61 LAPQORAPPOQRSSPSEGLCPGHHISEDRDCISCKYGQDYSTHWNDDLFCRLCTRCD 120
Db 121 SGEVELSPCTTTNTNTVOCCEGTFRDEDSPEMKCKRTGCGRGVAVGDDCTPMSDIECVH 180
121 SGEVELSPCTTTNTNTVOCCEGTFRDEDSPEMKCKRTGCGRGVAVGDDCTPMSDIECVH 180
Db 181 KESGTHSGEPAPAVEETVTSPTGTPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
181 KESGTHSGEPAPAVEETVTSPTGTPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
Db 181 KESGTHSGEPAPAVEETVTSPTGTPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
181 KESGTHSGEPAPAVEETVTSPTGTPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
Db 241 LPTKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSIILOPTQVPEQEMEVOEPAEPTGV 300
241 LPTKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSIILOPTQVPEQEMEVOEPAEPTGV 300
Db 241 LPTKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSIILOPTQVPEQEMEVOEPAEPTGV 300
241 LPTKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSIILOPTQVPEQEMEVOEPAEPTGV 300
Db 301 NMLSPGSEHLLPEPAERERORRLVLPANEGDPTETLRQCFFDFADLVFPDSWEPLMRK 360
301 NMLSPGSEHLLPEPAERERORRLVLPANEGDPTETLRQCFFDFADLVFPDSWEPLMRK 360
Db 301 NMLSPGSEHLLPEPAERERORRLVLPANEGDPTETLRQCFFDFADLVFPDSWEPLMRK 360
301 NMLSPGSEHLLPEPAERERORRLVLPANEGDPTETLRQCFFDFADLVFPDSWEPLMRK 360
Db 361 LGIMDNEIKYAKAEAGHDTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 420
361 LGIMDNEIKYAKAEAGHDTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 420
Db 421 HLISGKFMYLEGNADSAMS 440
421 HLISGKFMYLEGNADSAMS 440

RESULT 3
015508 PRELIMINARY; PRT; 411 AA.
ID 015508;
AC 015508;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE P53-REGULATED DNA DAMAGE-INDUCIBLE CELL DEATH RECEPTOR (FAS-LIKE
DE PROTEIN PRECURSOR).
GN KILLER OR DR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-OVARIAN;
RA Wu G.S., el-Deiry W.S.;
RL Nat. Genet. 16:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=97390508; PubMed=9242610;
RA Pan G., Ni J., Wei Y.F., Yu G., Gentz R., Dixit V.M.;
RT "An antagonist decoy receptor and a death domain-containing receptor
RT for TRAIL.";
RL Science 277:815-818(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Cao X., Zhang W., Wan T.;
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.

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DR EMBL: AF022386; AAB71949.1; -
DR EMBL: AF012628; AAB67109.1; -
DR EMBL: AF153687; AAF75587.1; -
DR HSSP: P19438; 1EXT.
DR INTERPRO: IPR000488; -
DR INTERPRO: IPR001368; -
DR PFAM: PF00020; TNR_C6; 2.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNR_NGFR_2; 2.
SO SEQUENCE 411 AA; 45083 MW; 57D50020E72CC954 CRC64;

Query Match 92.5%; Score 2151.5; DB 4; Length 411;
Best Local Similarity 93.4%; Pred. No. 2.5e-166;
Matches 411; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MEORGONAPASGARRKHGPGPREARGARPGVPKTLVVAVALLVSAESALITQOD 60
DB 1 MEORGONAPASGARRKHGPGPREARGARPGVPKTLVVAVALLVSAESALITQOD 60
QY 61 LAQOQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGQDYSTHNDLLFCLRCTCD 120
DB 61 LAQOQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGQDYSTHNDLLFCLRCTCD 120
QY 121 SGEVELSPCTTNTNTVQCCEGTFRFEDSPDMCKRCKRTGCPRGWVKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTNTNTVQCCEGTFRFEDSPDMCKRCKRTGCPRGWVKVGDCTPMSDIECVH 180
QY 181 KESGTHSGAPAVEETVTSPTGPASPCSLSGIIGVTAAVVAVVAVVCCKSLMKV 240
DB 181 KE-----SGIIGVTAAVVAVVAVVCCKSLMKV 211
QY 241 LPTLKIGICSGGGDPPEVDRSSORPGAEDNVLEIVSILOPTQVPEQEMVOEPAEPTGV 300
DB 212 LPTLKIGICSGGGDPPEVDRSSORPGAEDNVLEIVSILOPTQVPEQEMVOEPAEPTGV 271
QY 301 NMLSPGESEHLEPAAERQORRLVPANEGDPTELRQCFDFADLVFPDSWEPLMRK 360
DB 272 NMLSPGESEHLEPAAERQORRLVPANEGDPTELRQCFDFADLVFPDSWEPLMRK 331
QY 361 LGIMDNEIKAKAEAGHRTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 420
DB 332 LGIMDNEIKAKAEAGHRTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 391
QY 421 HLSSGKFWTLEGNADSAMS 440
DB 392 HLSSGKFWTLEGNADSAMS 411

RESULT 4
ID 014720 PRELIMINARY; PRT; 411 AA.
AC 014720;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE DEATH RECEPTOR 5.
GN DR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97390509; Pubmed=9242611;
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA Goddard A.D., Godowski P., Ashkenazi A.,
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT receptors."
RL Science 277:818-821(1997).

DR EMBL: AF012535; AAB67103.1; -
DR HSSP: P19438; 1EXT.
DR INTERPRO: IPR000488; -
DR INTERPRO: IPR001368; -
DR PFAM: PF00020; TNR_C6; 2.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNR_NGFR_2; 2.
SO SEQUENCE 411 AA; 45081 MW; 069BDD63CA608953 CRC64;

Query Match 91.9%; Score 2138.5; DB 4; Length 411;
Best Local Similarity 93.0%; Pred. No. 2.9e-165;
Matches 409; Conservative 1; Mismatches 1; Indels 29; Gaps 1;

QY 1 MEORGONAPASGARRKHGPGPREARGARPGVPKTLVVAVALLVSAESALITQOD 60
DB 1 MEORGONAPASGARRKHGPGPREARGARPGVPKTLVVAVALLVSAESALITQOD 60
QY 61 LAQOQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGQDYSTHNDLLFCLRCTCD 120
DB 61 LAQOQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGQDYSTHNDLLFCLRCTCD 120
QY 121 SGEVELSPCTTNTNTVQCCEGTFRFEDSPDMCKRCKRTGCPRGWVKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTNTNTVQCCEGTFRFEDSPDMCKRCKRTGCPRGWVKVGDCTPMSDIECVH 180
QY 181 KESGTHSGAPAVEETVTSPTGPASPCSLSGIIGVTAAVVAVVAVVCCKSLMKV 240
DB 181 KE-----SGIIGVTAAVVAVVAVVCCKSLMKV 211
QY 241 LPTLKIGICSGGGDPPEVDRSSORPGAEDNVLEIVSILOPTQVPEQEMVOEPAEPTGV 300
DB 212 LPTLKIGICSGGGDPPEVDRSSORPGAEDNVLEIVSILOPTQVPEQEMVOEPAEPTGV 271
QY 301 NMLSPGESEHLEPAAERQORRLVPANEGDPTELRQCFDFADLVFPDSWEPLMRK 360
DB 272 NMLSPGESEHLEPAAERQORRLVPANEGDPTELRQCFDFADLVFPDSWEPLMRK 331
QY 361 LGIMDNEIKAKAEAGHRTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 420
DB 332 LGIMDNEIKAKAEAGHRTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 391
QY 421 HLSSGKFWTLEGNADSAMS 440
DB 392 HLSSGKFWTLEGNADSAMS 411

RESULT 5
ID 015517 PRELIMINARY; PRT; 411 AA.
AC 015517;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOOXIC TRAIL RECEPTOR-2.
GN DR5 OR TRICK2A OR ZTNFR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Macfarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
RA Cohen G.M., Alnemri E.S.,
RL J. Biol. Chem. 0:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Sreteron G.R., Mongkolsapaya J., Xu X., Cowper A.E., McMichael A.J.,
RA Bell A.U.,
RL Curr. Biol. 0:0-0(1997).
RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE-98090092; PubMed-9430227;
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
 RT "Death receptor 5, a new member of the TNFR family, and Dd4 induce
 RT FADD-dependent apoptosis and activate the NF-kappaB pathway."
 RL Immunity 7:821-830(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Hood L.;
 RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Fairah T., Vu T., Gilbert T., Gross J., O'Hara P.;
 RT "Homo sapiens homolog of tumor necrosis factor receptor."
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF020501; AAB71412.1; -;
 DR EMBL: AF018657; AAB70577.1; -;
 DR EMBL: AF016268; AAC01565.1; -;
 DR EMBL: AF192548; AAF07175.1; -;
 DR HSSP: P19438; TEXT.
 DR INTERPRO: IPR000488; -;
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PFAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR RECEPTOR.
 SO SEQUENCE 411 AA; 45127 MW; D76A1C9B2FC747F9 CRC64;

Query Match 91.9%; Score 2137.5; DB 4; Length 411;
 Best Local Similarity 93.0%; Pred. No. 3.5e-165;
 Matches 409; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

QY 1 MGRCGNAAASGARRHGPGRPREANGARPPRPVPTLVVAVALLLVSAESALITQOD 60
 DB 1 MGRCGNAAASGARRHGPGRPREANGARPPRPVPTLVVAVALLLVSAESALITQOD 60
 QY 61 LAPQRAAPQOKRSSPSEGLCPGHHIISDGRDCISCKTGODSTHWNLLFCLRCTG 120
 DB 61 LAPQRAAPQOKRSSPSEGLCPGHHIISDGRDCISCKTGODSTHWNLLFCLRCTG 120
 QY 121 SGEVELSPCTTTRNTVCCGEEGTFREDSPEMCKRCRTGCPRGWVVGCTPMSDIECVH 180
 DB 121 SGEVELSPCTTTRNTVCCGEEGTFREDSPEMCKRCRTGCPRGWVVGCTPMSDIECVH 180
 QY 181 KESGTHSEAEAVETVTSFGTPASPCSLGIIGTVAAVVLIVAVFVCKSLMKRV 240
 DB 181 KE-----SGIIGTVAAVVLIVAVFVCKSLMKRV 211
 QY 241 LPYLKIGCGGGGDPPEVRDSSORPGADNVLAIEYSILOPTOVPEQMEVGPAPPTGV 300
 DB 212 LPYLKIGCGGGGDPPEVRDSSORPGADNVLAIEYSILOPTOVPEQMEVGPAPPTGV 271
 QY 301 NMLSPGSESHLLEPAEERSQRRLLVANEGDPTETLLRQCFDDFADLVPFDSWPELMRK 360
 DB 272 NMLSPGSESHLLEPAEERSQRRLLVANEGDPTETLLRQCFDDFADLVPFDSWPELMRK 331
 QY 361 LGIMNEIKVAAGAAAGHDTLYTMLIKVNTGGRASVHTLLDALETLGERLAKOKID 420
 DB 333 LGIMNEIKVAAGAAAGHDTLYTMLIKVNTGGRASVHTLLDALETLGERLAKOKID 391
 QY 421 HLSSGKFMYLEGNADSAMS 440
 DB 392 HLSSGKFMYLEGNADSAMS 411

RESULT 6
 ID 000220 PRELIMINARY; PRT: 468 AA.
 AC 000220;
 DT 01-JUL-1997 (TREMblrel. 04, Created)

DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE CYTOTOXIC LIGAND TRAIL RECEPTOR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97238921; PubMed-9082980;
 RA Pan G., O'Rourke K., Chinaiyan A.M., Gentz R., Ebnner R., Ni J.,
 RA Dixit V.M.;
 RT "The receptor for the cytotoxic ligand TRAIL."
 RT Science 276:1111-1133(1997).
 RL EMBL: U90875; AAC51226.1; -;
 DR HSSP: P19438; TEXT.
 DR INTERPRO: IPR000488; -;
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PFAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR RECEPTOR.
 SO SEQUENCE 468 AA; 50025 MW; 1E85DCDC2C8760F7 CRC64;

Query Match 45.6%; Score 1061.5; DB 4; Length 468;
 Best Local Similarity 52.0%; Pred. No. 5.8e-78;
 Matches 234; Conservative 41; Mismatches 118; Indels 57; Gaps 8;

QY 5 GONAPASGARRHGPGRPREANGARPPRPVPTLVVAVALLLVSAESALITQODLAP 63
 DB 60 GGHGGSAR-ARRGRAPGRPAEASPRLVHHTFFVVGVLQVVPSSANTIKHID--- 115
 QY 64 GQRAAPQOKRSSPSEGLCPGHHIISDGRDCISCKTGODSTHWNLLFCLRCTGDSGE 123
 DB 116 -OSIGTQWEHSPLELCPGSGHRSERPGACNRCETGEGYTNASNNLFCACPCTACKSDE 174
 QY 124 VELSPCTTTRNTVCCGEEGTFREDSPEMCKRCRTGCPRGWVVGCTPMSDIECVHES 183
 DB 175 EERSPCTTTRNTACCKRTGTFRNDNSAEKRCSTGCGRGWVVGCTPMSDIECVHES 234
 QY 184 GTHSGEAPAVEETVTSFGTPASPCSLGIIGTVAAVVLIVAVFVCKSLMKVLPY 243
 DB 235 GNGHN-----IWLIVTVTLVPLLVAVL----- 259
 QY 244 LKGI-----SGGGDPPEVRDSS-----QRPAGEDNVLAIEYSILO--PTOVPEQME 290
 DB 260 ---VCCIGSGGGGDPKCMKDFWRLGLRPGADNVAHNEILSNADSLSTFVSEQOME 316
 QY 291 VOEPAPPTGVNMLSPGSESHLLEPAEERSQRRLLVANEGDPTETLLRQCFDDFADLVP 350
 DB 317 SOEPADLTGVYVSQGEACCLGPRAEAGSORRLLVANAGADPTETLLMFFDFANIVP 376
 QY 351 FDSWPELMRKLGIMNEIKVAAGAAAGHDTLYTMLIKVNTGGRASVHTLLDALETLG 410
 DB 377 FDSWQLMRKOLDLTNEIDIVVAGTAGGADLYAMLKMWKNTGGRASVHTLLDALELME 436
 QY 411 ERLAKOKIEDHLSSGKFMYLEGNADSAMS 440
 DB 437 ERHAKEKIDLLVDSGKPYLEDGTGSAYS 466

RESULT 7
 ID 09UBN6
 AC 09UBN6; PRELIMINARY; PRT: 386 AA.
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE DECOY RECEPTOR 2.
 GN TRAIL-R4.
 OS Homo sapiens (Human).

RESULT 9
 O9QZM4 PRELIMINARY; PRT; 381 AA.
 ID O9QZM4
 AC O9QZM4
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, last annotation update)
 DE KILLER/DR5 TRAIL DEATH-INDUCING RECEPTOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCB1_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99310501; PubMed-10383128;
 RA Wu G.S., Burns T.E., Zhan Y., Alnemri E.S., El-Deiry W.S.;
 RT "Molecular cloning and functional analysis of the mouse homologue of
 RT the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand
 RT (TRAIL) death receptor."
 RL Cancer Res. 59:2770-2775(1999).
 DR EMBL: AF176833; AAD52656.1; -;
 DR INTERPRO: IPR000468; -;
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNR_C6; 2.
 DR PFAM: PF00531; death. 1.
 DR PROSITE: PS00652; TNR_NGFR.1; UNKNOWN_2.
 DR PROSITE: PS50017; DEATH_DOMAIN. 1.
 DR PROSITE: PS50050; TNR_NGFR_2; 2.
 KM Receptor.
 SQ SEQUENCE 381 AA; 42164 MW; 22531758F4ADE0A CRC64;

Query Match 25.3%; Score 588; DB 11; Length 381;
 Best Local Similarity 34.3%; Pred. No. 1e-39;
 Matches 148; Conservative 67; Mismatches 148; Indels 68; Gaps 10;

QY 1 MEORGNAPASGARKRHPGPREARGARPPVKTLYVVAVLLVSAESALITQOD 60
 DB 1 MEPPGSTPTASAAARADHYTP---GLRP---LRRLLYSFALLMLAQAVFVPVTPAN 53
 QY 61 LAPQORAPQOKRSSPSEGLCPPGHHISDGDICISCKYGDYSTHMDLL-FCLRCTRC 119
 DB 54 PAHNRPAQIQRREESPSRGPCLAGYLSEG--NCKPCREGIDYTSNHSNLSLCTCTVC 111
 QY 120 DSGEVELSPCTTNTNTVQCCGEGTFREEDSPMCKRCRTGCGRGWVGVDCPTMSDIECV 179
 DB 112 KEDKVVETRCNTTNTVYCRCKPGTFEDKDSPEICQSC-SNCTDGEELTSCPTRENKCV 170
 QY 180 HKESGTRKSGEAPAVEETVTSPPGSPASCSLSGIIIGVYAAVLLVAVFYCKSLMK 239
 DB 171 SK-----TAMASWHLGLMIGLIVPVVLLIGALLVWTKGAMRQ 208
 QY 240 VLPYKLGICSGGGGPERVDRSSORPGAEDNVLEIVSLIOPVQEGEVEQPAEPTG 299
 DB 209 WLCTKRGE--RDPESA-----NSVHSLIDRQTS-- 238
 QY 300 VMLSPGESEHLEPAEAERSORRLVLPANEGDPTETLRQCFDPAFLVPDPSWEPLMR 359
 DB 239 ----TTNDSNHNTEPGKQKT-GKKLLVPVNGNDSADDLKTFEFCSDIIVPDSWNRMLR 293
 QY 360 KLGLMDNEIKYAKAEAGHRDTLYTMLIKWVKTKGRDASVHTLLDALETIGERLAKOKIE 419
 DB 294 QUGLNDNOIOWKAEITLVTRALYOMLKWHRQGRSASINHLDDALEAVEERDAMEKIE 353
 QY 420 DHLLSGKFWY 430
 DB 354 DYAVKSGRFTY 364

RESULT 10
 O9JUI6

ID O9JUI6 PRELIMINARY; PRT; 381 AA.
 AC O9JUI6
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
 DE TRAIL RECEPTOR KILLER/DR5 HOMOLOGUE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCB1_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=SPLEEN.
 RA Nakamura Y., Tamari M., Watanabe O.;
 RT "Mouse TRAIL receptor."
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB031081; BAA96462.1; -;
 KM Receptor.
 SQ SEQUENCE 381 AA; 42223 MW; 2E7999EA2EB485B1 CRC64;

Query Match 24.9%; Score 580; DB 11; Length 381;
 Best Local Similarity 33.9%; Pred. No. 4.5e-39;
 Matches 146; Conservative 69; Mismatches 148; Indels 68; Gaps 11;

QY 1 MEORGNAPASGARKRHPGPREARGARPPVKTLYVVAVLLVSAESALITQOD 60
 DB 1 MEPPGSTPTASAAARADHYTP---GLRP---LRRLLYSFALLMLAQAVFVPVTPAN 54
 QY 61 LAPQORAPQOKRSSPSEGLCPPGHHISDGDICISCKYGDYSTHMDLL-FCLRCTRC 119
 DB 55 -AHNRPAQIQRREESPSRGPCLAGYLSEG--NCKPCREGIDYTSNHSNLSLCTCTVC 111
 QY 120 DSGEVELSPCTTNTNTVQCCGEGTFREEDSPMCKRCRTGCGRGWVGVDCPTMSDIECV 179
 DB 112 KEDKVVETRCNTTNTVYCRCKPGTFEDKDSPEICQSC-SNCTDGEELTSCPTRENKCV 170
 QY 180 HKESGTRKSGEAPAVEETVTSPPGSPASCSLSGIIIGVYAAVLLVAVFYCKSLMK 239
 DB 171 SK-----TAMASWHLGLMIGLIVPVVLLIGALLVWTKGAMRQ 208
 QY 240 VLPYKLGICSGGGGPERVDRSSORPGAEDNVLEIVSLIOPVQEGEVEQPAEPTG 299
 DB 209 WLCTKRGE--RDPESA-----NSVHSLIDRQTS-- 238
 QY 300 VMLSPGESEHLEPAEAERSORRLVLPANEGDPTETLRQCFDPAFLVPDPSWEPLMR 359
 DB 239 ----TTNDSNHNTEPGKQKT-GKKLLVPVNGNDSADDLKTFEFCSDIIVPDSWNRMLR 293
 QY 360 KLGLMDNEIKYAKAEAGHRDTLYTMLIKWVKTKGRDASVHTLLDALETIGERLAKOKIE 419
 DB 294 QUGLNDNOIOWKAEITLVTRALYOMLKWHRQGRSASINHLDDALEAVEERDAMEKIE 353
 QY 420 DHLLSGKFWY 430
 DB 354 DYAVKSGRFTY 364
 RESULT 11
 ID O9JUI5 PRELIMINARY; PRT; 385 AA.
 AC O9JUI5
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
 DE TRAIL RECEPTOR2 KILLER/DR5 HOMOLOGUE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCB1_TaxID=10090;
 [1]


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Db      53 ANDSIQCLPK-KDEYTERPNDPKKICGCTCREDQVEVSPICPTRTQCAKNGTFCLP 111
      148 DSP-EMCRKCRGTCGPGMVGSDCTPMSDIECHKSGTGHSEDAVAEVTIVSSGTPTA 206
      112 DHCECMQCKQTCPCPGVNLAPCTQHSDLCC-----GPLE- -ISSSSST- 155
      207 SPSCSGIITGVVAVAVLVAVVCKSLMKFVLYLKIGCS-----GGGGDEPR----- 257
      156 -----LMIITFFVLAVILGLV-----FWKR-----CSSRHGAGDDDELMSKPS 198
      258 --VDRSSQRPAGADNVLNEIVSLPTQVPEOMEVQEPAPETPGVNMSPGSEHLLPEA 315
      199 AVVNRLLQRLQIGIDNRCNE--QIYQNOQOQELFTAGQSEVPHGVM--EGTERRTPD- 253
      316 EAMRSQRRLLVPANSGDPTETLRQCFDDFADIVPPDSMEPLMRKICLIMDNELKAKAEA 375
      254 ---KVTQKRLVAVLGENPAILHRSFNFTVDYPPPEMKRFGRALDLQENDLYLAQHD 310
      376 AGHRDLVYMLIKVWKTKGRDASVHTLLDALLETIGERLAKQKIEDHLLSSGKPMY 430
      311 RVSCEFFYQMLNWTNLNQGSKASVNTLLETLPRIIGLGVADIIASFLISKGYQY 365

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RESULT 14
014798 PRELIMINARY; PRT: 299 AA.
AC 014798:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CYTOTOXIC TRAIL RECEPTOR-3 (LYMPHOCYTE INHIBITOR OF TRAIL) (ANTAGONIST
DE DECOY RECEPTOR FOR TRAIL/APO-2L).
GN TRAIL-R3 OR LIT OR TRID OR DCRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
RA Cohen G.M., Alnemri E.S.,
RA J. Biol. Chem. 0:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Degli-Esposti M.A., Smolak P.J., Walczak H., Naught J., Huang C.P.,
RA Dubose R.F., Goodwin R.G., Smith C.A.,
RA "Cloning and characterization of TRAIL-R3, a novel member of the
RT emerging TRAIL receptor family."
RT J. Exp. Med. 186:1165-1170(1997).
RN [3]
RP SEQUENCE OF 41-299 FROM N.A.
RA Mongkolsapaya J., Cowper A., Xu X., Morris G., McMichael A.J.,
RA Bell J.I., Screaton G.R.,
RA J. Immunol. 0:0-0(1997).
RN [4]
RP SEQUENCE OF 41-299 FROM N.A.
RA MEDLINE=97390508; PubMed=9242610;
RA Pan G., Ni J., Wei Y.F., Yu G., Gentz R., Dixit V.M.,
RA "An antagonist decoy receptor and a death domain-containing receptor
RT for TRAIL."
RT Science 277:815-818(1997).
RN [5]
RP SEQUENCE OF 41-299 FROM N.A.
RA MEDLINE=97390509; PubMed=9242611;
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA Goddard A.D., Godowski P., Ashkenazi A.,
RA "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT receptors."
RT Science 277:818-821(1997).
DR EMBL; AF020502; AAB71413.1; -

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DR EMBL; AF014794; AAC05593.1; -
DR EMBL; AF033854; AAB87506.1; -
DR EMBL; AF012629; AAB67110.1; -
DR EMBL; AF012536; AAB67104.1; -
DR HSP; P19438; TEXT.
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_c6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00505; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 299 AA; 31759 MW; 2435106F847FF1AB CRC64;

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Query Match 20.1%; Score 467; DB 4; Length 299;
Best Local Similarity 39.2%; Pred. No. 4,7e-30;
Matches 112; Conservative 25; Mismatches 87; Indels 62; Gaps 4;

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QY 5 GONAPASGARRKHGPGPREARGARPPVPTL--VLVVAALLVSAESALITQODLA 62
      15 GBRAPRPDGRGRVRRPTQDGVGNHTMARIPKTLFVVVYVAVLLPLAYSATTAEEV 74
      63 PQRAAPQQRKSSPSRGLCPRGHHISEGRCDCISCKYGODYSTHNNDLFLCRLCRCSG 122
      75 PQOTVAPQQRHSFSGECPAGSHRSEHTGACNPCTEGVDYTNASNNBSPCPTVCKSD 134
      123 EVELSPCTTTRNTVCCCEGTFRFEDSPEMCRKCRGCGPRGAVKGDCTPMSDIECVH-- 180
      135 QKHSSCTITRDTVCCQCKGRTFRNENSPMCKKC--SRCPGEGVQVSNCTSWDDICVEEF 193
      181 -----KESG 184
      194 GNAATVETPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETM 253
      185 TKHSG-EAPAVEETVTSRGTASCSLSGIIITGVVAVLIYAV 229
      254 TTSPTGPAPAAEETMTSPGTPASSHYLSCTIVGIIIVLILVYV 299

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RESULT 15
09PW79 PRELIMINARY; PRT: 368 AA.
AC 09PW79:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE TVB3.
GN TVB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Brojatsch J., Naughton J., Rolis M.M., Zingler K., Young J.A.,
RA Brojatsch J., Naughton J.,
RA "CARL, a TNFR-related protein, is a cellular receptor for cytopathic
RT avian leukosis-sarcoma viruses and mediates apoptosis."
RT Cell 87:845-855(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Brojatsch J., Naughton J., Young J.A.,
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RT EMBL; AF161712; AAD47256.1; -
DR HSP; P19438; TNFR.
DR INTERPRO; IPR000488; -
DR INTERPRO; IPR001368; -
DR INTERPRO; IPR001450; -
DR PFAM; PF00020; TNFR_c6; 2.
DR PFAM; PF00531; death_1.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.

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DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 368 AA; 41515 MW; F558C225AB3750BB CRC64;

Query Match 20.0%; Score 464.5; DB 13; Length 368;

Best Local Similarity 32.8%; Pred. No. 9.7e-30;
Matches 136; Conservative 50; Mismatches 158; Indels 71; Gaps 14;

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QY 36 KTVLVVAALVVAASALITQODLAPQORAPPOKRSSPSE-----GLCPGCHI 87
DB 2 RSAALRLCPVLLLFPAVOL-----GSAALVKKRADSDLOKPDLYRRKCPMGTYE 52
QY 88 SEDGRDCISCKYGQDYSTHWNDDLFLCLRCTRCDSGEVELSPCTTNTNTVQCCEGTFREE 147
DB 53 ANDSIOCLPSK-KDEYTEYNDPFPKICGCRTEHQDQEVESPCIPTRNTQCACKNGTFCLP 111
QY 148 DSP-EMCRKCRCTGCPRGKAVGDCITPMSDIECVHKEGSKHSGEAPAVETVTSPTPA 206
DB 112 DHPCEMCKQCKQTECPKGOVRLAPCTOHSDLLC-----GPPLE--ISSSST-- 155
QY 207 SPCSLSGIITGVVAAVLIVAVFVCKSLMKVLPYLKIGCS---GGGDPER----- 257
DB 156 -----LMIITTFVLAVIIGLVV----FWKR-----CSSRHGAGDDDELSTKPS 198
QY 258 --VDRSSQRPAGADNYLNEIVSIIPTQVPEQEMEVQEPAPETGVNMLSPGESEHLEPA 315
DB 199 AVVNRLLQRLGIQDNRCNE--QIYQNOQOQELLETAGSEVPHGVEH--EGTERRTDP- 253
QY 316 EARSQRRRLVPAANGDPETETLRQCFDDPADLVFPDSEPLMRKLGIMDNEIKVAKAEA 375
DB 254 --KVEIQRLVPLVGENPIALHRSFNTPVDVPPPEWKRFGRAIDLQENDLYLAEQHD 310
QY 376 AGHROTLTYMLIKVWNKGRDASVHTLLDALLETGERLAKQIEDHLLSSGKFMV 430
DB 311 RVSCPEPYQMLNTWLNQOGSKASVNTLETLPRIGLSGVADITASELISKGYQY 365
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Job time: 89 sec

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